

AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

Claims 1-24. (Canceled)

25. (Previously Presented) An isolated Hepatitis C virus polynucleic acid selected from the group consisting of:

- (i) the nucleotide sequence of SEQ ID NO:147,
- (ii) at least 8 contiguous nucleotides of a nucleotide sequence having at least one genotype-specific nucleotide from the region spanning positions 1 to 346 of the Core -region of HCV subtype 3c, and,
- (iii) the complement of the nucleotide sequence of (i) or (ii).

Claim 26. (Canceled)

27. (Previously Presented) A recombinant vector comprising a vector sequence and a prokaryotic, eukaryotic or viral promotor sequence operably linked to a polynucleic acid sequence of claim 25.

Claim 28. (Canceled)

29. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

- (i) providing a sample nucleic acid,
- (ii) determining the presence of a polynucleic acid sequence according to claim 25, by means of a sequencing reaction, and,
- (iii) inferring from the presence of one or more of these HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

Claim 30. (Canceled)

31. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

- (i) providing a sample nucleic acid,
- (ii) specifically amplifying a polynucleic acid sequence according to claim 25, and,
- (iii) inferring from the presence of one or more amplified HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

Claims 32-34. (Canceled)

35. (Currently Amended) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a primer of a HCV subtype 3c nucleic acid sequence, and wherein said polynucleic acid comprises at least one HCV subtype 3c genotype specific nucleotide~~consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.~~

Claim 36. (Canceled)

37. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV type or subtype-specific, and wherein said polynucleic acid consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.

Claim 38. (Canceled)

39. (Currently Amended) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV subtype 3c nucleic acid sequence, and wherein said polynucleic acid comprises at least one HCV subtype 3c genotype specific nucleotide~~consists of up to 50 contiguous nucleotides selected from said HCV subtype 3c genomic region.~~

Claim 40. (Canceled)

41. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a polynucleic acid sequence according to claim 25.

Claims 42-44. (Canceled)

45. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 35.

Claim 46. (Canceled)

47. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 37.

Claim 48. (Canceled)

49. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 39.

Claims 50-52. (Canceled)

53. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

- (i) providing a sample nucleic acid,
- (ii) amplifying the nucleic acid with at least one primer according to claim 35,
- (iii) detecting the amplified nucleic acids,
- (iv) inferring the presence of one or more genotypes of HCV present from the observed pattern of amplified fragments.

Claim 54. (Canceled)

55. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

- (i) providing a sample nucleic acid,
- (ii) optionally amplifying the nucleic acid with at least one primer,
- (iii) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 37, with said probes being optionally attached to a solid substrate,
- (iv) optionally washing,
- (v) detecting the hybrids formed,
- (vi) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

Claim 56. (Canceled)

57. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

- (i) providing a sample nucleic acid,
- (ii) optionally amplifying the nucleic acid with at least one primer,
- (iii) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 39, with said probes being optionally attached to a solid

substrate,

(iv) optionally washing,

(v) detecting the hybrids formed,

(vi) inferring the presence of one or more genotypes of HCV present from the
observed hybridization pattern.